

	10	20	30	40	50	60
SEQIDNO:1 5789228	ATGATAAACGTTGCAACGGGAGAGGAGACCCCAATACACCTCTTTGGAGTCAACTGGTTC					
SEQIDNO:45 09/914543	atga-----gcaa--gaaaa-agttcgatcat-cgtatctatc--ttaacaa--tc					
	70	80	90	100	110	120
SEQIDNO:1 5789228	GGCTTTGAG-ACACCGAACTAGGTTCTTCACGGCCTATGGAGTAGCAACTGGGAGGA-CA					
SEQIDNO:45 09/914543	--cttttagtacaggcaa-ta--tatt-----t-t--gtagaaa--agtatca					
	130	140	150	160	170	180
SEQIDNO:1 5789228	TGCTCCTCCAGATCAAGAGCCTTGGCTTCAATGCGATAAGGCTTCCCTTCTGTACCCAGT					
SEQIDNO:45 09/914543	tacctctgagga-caag-----tcaacttcaa--ata-----cct-----ca-t					
	190	200	210	220	230	240
SEQIDNO:1 5789228	CAGTAAACCGGGGACCATGCCAACGGCGATTGACTACGCCAAGAACCAGACCTCCAGG					
SEQIDNO:45 09/914543	c--taca--cc-----acc-----ccaaa--caac--acttt--ccacta--cca-----agg					
	250	260	270	280	290	300
SEQIDNO:1 5789228	GTCTTGACAGCGTCCAGATAATGGACAAAATAATCAAGAAAGGCTGGAGACCTGGGCATAT					
SEQIDNO:45 09/914543	ttct--ca-----agatta--gataccctgat--gacgg--tg--ag--tggc--ag--					
	310	320	330	340	350	360
SEQIDNO:1 5789228	TCGTGCTCCTCGA-CTACCACAGAATAGGATGCAACTTCATAGAACCCCTATGGTACACCG					
SEQIDNO:45 09/914543	--gagctcct--att-----gataaggatgg-----t-ga-----tggga--acc					
	370	380	390	400	410	420
SEQIDNO:1 5789228	ACAGCTTCTCGGAGCAG-GACTACATAAACACCTCGGTTGAAGTCGCCAGAGGTTGGGC					
SEQIDNO:45 09/914543	agaa--ttct--a--cattga--a--ataaac--ctatg--gaa-----ca--ttctta					
	430	440	450	460	470	480
SEQIDNO:1 5789228	AAG-TACTGGAACGTTATCGGCGCGGACCTGAAGAACGAACCCACAGCTCAAGCCCCGC					
SEQIDNO:45 09/914543	atgctactgga--tt-t--gctga--gatga--cgtac-----aatttaa--ccagc					
	490	500	510	520	530	540
SEQIDNO:1 5789228	ACCTGCCCGCTTACACTGACGGAAGTGGGGCCACGTGGGGAATGGGCAACAACGCCACCGA					
SEQIDNO:45 09/914543	g--ggtccttcaact-----acgtc-----caacaactt--ga					
	550	560	570	580	590	600
SEQIDNO:1 5789228	CTGGAACCTGGCGGCTGAGAGGATAGGAAGCGCAATTCTGGAGGTGCCCCACAATGGGT					
SEQIDNO:45 09/914543	c--aacattgtct--tgag--ggatag--aagt--aatt-----gggtgc-----atgg--					
	610	620	630	640	650	660
SEQIDNO:1 5789228	TATATTTGTTGAGGGAACCCAGTTTACCACCCCCGACATAGACGGTAGGTACAAGTGGGG					
SEQIDNO:45 09/914543	-ata-----ccccgaata-----ttcta--tgg--					
	670	680	690	700	710	720
SEQIDNO:1 5789228	CCACAACGCCTGGTGGGGCGGAACCTTATGGGTGTTAGGAAGTACCCAGTTAACCTGCC					
SEQIDNO:45 09/914543	--a-aac-----aagcc--atgg-----aa--tgc-----aaactacg					
	730	740	750	760	770	780
	.....					

SEQIDNO:1 5789228 CAGGGACAAGGTTGTTTACAGCCCCAAGTTTACGGTTCAGAAGTTTACGACCAGCCCTA  
 SEQIDNO:45 09/914543 ca---ac---tgat---ggccc---aa---tac---ca---ttac---ccag---ta

790 800 810 820 830 840  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CTTTGACCCCGGTGACGGGTTCCCCGACAACCTCCCCGAAATATGGTACCACTACTTCGG  
 SEQIDNO:45 09/914543 -----aag---tttc---a---aacct-----aa-----cag---acttc---

850 860 870 880 890 900  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CTACCTAAAGCTTGATCTCGGTTACCTCTTGTATAGGTGAGTTCCGAGGCAAGTACGG  
 SEQIDNO:45 09/914543 -tatctaa---ca---atctc-----ctat---aaacttgag---cc---caagaacgg

910 920 930 940 950 960  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CCATGGGGGAGACCCGAGGATGTCACCTGGCAGAACAGATAATAGACTGCATGATCCA  
 SEQIDNO:45 09/914543 cc---tg-----cc---a---at---taacttcgca-----atagaatc---ctgggttaa---cga

970 980 990 1000 1010 1020  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 GAACAAATTCGTGACTTCTTCTACTGGAGCTGGAAACCAAACAGCGGTGACACCGGTGG  
 SEQIDNO:45 09/914543 gag---aagct---tg---gaga-----ac---aacaggaatt---aacagcgatga---gcaag

1030 1040 1050 1060 1070 1080  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 AATTCTGAAGGATGACTGGACGACAATATGGGAGGACAAGTACAACAACCTGAAGAGGCT  
 SEQIDNO:45 09/914543 aagt---aatgat---a---tggattt---actatg-----ac---ggattacaaccggctg---gct

1090 1100 1110 1120 1130 1140  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CATGGAACAGCTGTTCTGGAAACGCCACTGCCCGCTCGTCCCCACGACAACCTACAACAAC  
 SEQIDNO:45 09/914543 cc---aaag---ttaagga---g---attg-----ta---gtccc-----aat

1150 1160 1170 1180 1190 1200  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 AAGCAACCCGCCAACGACCACAACGACTACAACATCCAATCCAAACGACCACTACCCAGAC  
 SEQIDNO:45 09/914543 a---ata---gttaacg-----ga-----aca---ccagta---aatg---ctac-----

1210 1220 1230 1240 1250 1260  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CCCGACCACCACTACTCCAACCTACGACAACCAACCAGCACCACAACCTCCTTCAAATAACGT  
 SEQIDNO:45 09/914543 -----atttgaagtatgg---aagg---ca---a---acat---tgggttgggagtatgt

1270 1280 1290 1300 1310 1320  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CCCATTTGAAATTGTGAACGTTCTCCCCACTAGCTCCCGTACGAGGGAACCAGCGTGA  
 SEQIDNO:45 09/914543 tgcatttagaat---aaaga---cccc---a---t---ca---aagagggaac-----a

1330 1340 1350 1360 1370 1380  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 GGTGTATGTGATGGAACCACTGTGCCTCCAGCGTTTGGGGAGCTCCGAACCTCTGGGG  
 SEQIDNO:45 09/914543 g-----tga-----caat---tcca-----tacggagc-----atttata---

1390 1400 1410 1420 1430 1440  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 AGTCGTTAAATCGGAACGCCACCATGGAACCCAACGTTTGGGCTGGGAGGACGTTTA  
 SEQIDNO:45 09/914543 agt---gtt-----gc-----ag---ccaacattt---c-----aagctta

1450 1460 1470 1480 1490 1500  
 .....|.....|.....|.....|.....|.....|  
 SEQIDNO:1 5789228 CAAGACTGCACCCCAAGCAATTGGAACCGGCAGCACAAAGATGGAGATAAGGAACGGGGT  
 SEQIDNO:45 09/914543 ccaaatcac---agaacttt---acttagaggac---g---tggagat---ggaac---t

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1510      1520      1530      1540      1550      1560
SEQIDNO:1 5789228 GCTCAAGGTTACAAACCTCTGGAACATCAACATGCATCCGAAGTATAACACAATGGCATA
SEQIDNO:45 09/914543 g----ag--tt-----tggaacgc--caa--gca--c-----taccttc--gcca

1570      1580      1590      1600      1610      1620
SEQIDNO:1 5789228 CCCGAGGTCATATACGGCGCCAAGCCTTGGGGCAACCAGCCAATAAACGCTCCGAACCTT
SEQIDNO:45 09/914543 cctagag-----t--gg-----tggatca--caaaca--taa--cact--aact--

1630      1640      1650      1660
SEQIDNO:1 5789228 CGTGCTCCGATAAAGGTCTCCCAGCTTCCGAGGATACTTCGTTGA
SEQIDNO:45 09/914543 c---ctctagatagac--ctc-----tt-----at--ttccta--a

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